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        RAW SEQUENCE LISTING                 DATE: 11/27/2001
        PATENT APPLICATION:  US/09/852,370A  TIME: 10:36:53

        Input Set : N:\Crf3\RULE60\09852370A.RAW.txt
        Output Set: N:\CRF3\11272001\I852370A.raw
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 3 <110> APPLICANT: Pomerantz, Joel L.
 4          Sharp, Phillip A.
 5          Pabo, Carl O.
 7 <120> TITLE OF INVENTION: Chimeric DNA-binding proteins
 9 <130> FILE REFERENCE: APV-022.02
12 <140> CURRENT APPLICATION NUMBER: 09/852,370A
13 <141> CURRENT FILING DATE: 2001-05-10
15 <150> PRIOR APPLICATION NUMBER: 08/973,131
16 <151> PRIOR FILING DATE: 1997-11-26
18 <150> PRIOR APPLICATION NUMBER: PCT/US95/16982
19 <151> PRIOR FILING DATE: 1995-12-29
21 <150> PRIOR APPLICATION NUMBER: 08/366,083
22 <151> PRIOR FILING DATE: 1994-12-29
24 <160> NUMBER OF SEQ ID NOS: 75
26 <170> SOFTWARE: PatentIn Ver. 2.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 26
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Description of Artificial Sequence:
35      oligonucleotide used to determine the consensus
36      binding sequence of ZFHD1
38 <400> SEQUENCE: 1
39 gtttggcacc tgactaattt aaggag                              26
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 25
44 <212> TYPE: DNA
45 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
48 <223> OTHER INFORMATION: Description of Artificial Sequence:
49      oligonucleotide used to determine the consensus
50      binding sequence of ZFHD1
52 <400> SEQUENCE: 2
53 gcgttaatta agggaggtaa ggccc                               25
56 <210> SEQ ID NO: 3
57 <211> LENGTH: 25
58 <212> TYPE: DNA
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Description of Artificial Sequence:
63      oligonucleotide used to determine the consensus
64      binding sequence of ZFHD1
66 <400> SEQUENCE: 3
67 ctcggccgtt aatgaggggt gttcg                               25
70 <210> SEQ ID NO: 4
71 <211> LENGTH: 25
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 73 <213> ORGANISM: Artificial Sequence
 75 <220> FEATURE:
 76 <223> OTHER INFORMATION: Description of Artificial Sequence:
 77       oligonucleotide used to determine the consensus
 78       binding sequence of ZFHD1
 80 <400> SEQUENCE: 4
 81 taattatggg cgggatcgaa tagcc                                    25
 84 <210> SEQ ID NO: 5
 85 <211> LENGTH: 26
 86 <212> TYPE: DNA
 87 <213> ORGANISM: Artificial Sequence
 89 <220> FEATURE:
 90 <223> OTHER INFORMATION: Description of Artificial Sequence:
 91       oligonucleotide used to determine the consensus
 92       binding sequence of ZFHD1
 94 <400> SEQUENCE: 5
 95 ggcaataatc aatcctttaa ttatgg                                   26
 98 <210> SEQ ID NO: 6
 99 <211> LENGTH: 26
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence:
105       oligonucleotide used to determine the consensus
106       binding sequence of ZFHD1
108 <400> SEQUENCE: 6
109 ggccgtacct catgaaatta ggggcg                                   26
112 <210> SEQ ID NO: 7
113 <211> LENGTH: 25
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence:
119       oligonucleotide used to determine the consensus
120       binding sequence of ZFHD1
122 <400> SEQUENCE: 7
123 gttaattatg gggtaataat ggtgc                                    25
126 <210> SEQ ID NO: 8
127 <211> LENGTH: 25
128 <212> TYPE: DNA
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Description of Artificial Sequence:
133       oligonucleotide used to determine the consensus
134       binding sequence of ZFHD1
136 <400> SEQUENCE: 8
137 gtcgggctct gttaattatg ggtgg                                    25
140 <210> SEQ ID NO: 9
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Output Set: N:\CRF3\11272001\I852370A.raw

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141 <211> LENGTH: 25
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: Description of Artificial Sequence:
147       oligonucleotide used to determine the consensus
148       binding sequence of ZFHD1
150 <400> SEQUENCE: 9
151 ggataattac gggtggcatt taggc                                    25
154 <210> SEQ ID NO: 10
155 <211> LENGTH: 25
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Description of Artificial Sequence:
161       oligonucleotide used to determine the consensus
162       binding sequence of ZFHD1
164 <400> SEQUENCE: 10
165 gataaatagg ggcgtcccat cccgt                                    25
168 <210> SEQ ID NO: 11
169 <211> LENGTH: 24
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence:
175       oligonucleotide used to determine the consensus
176       binding sequence of ZFHD1
178 <400> SEQUENCE: 11
179 taaattaggg ctttaattac ggtc                                     24
182 <210> SEQ ID NO: 12
183 <211> LENGTH: 25
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence:
189       oligonucleotide used to determine the consensus
190       binding sequence of ZFHD1
192 <400> SEQUENCE: 12
193 tcattagagt gttaatgaga tgcgc                                    25
196 <210> SEQ ID NO: 13
197 <211> LENGTH: 26
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Description of Artificial Sequence:
203       oligonucleotide used to determine the consensus
204       binding sequence of ZFHD1
206 <400> SEQUENCE: 13
207 tagttgctaa tttgtattaa ttaaag                                   26
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Input Set : N:\Crf3\RULE60\09852370A.RAW.txt
Output Set: N:\CRF3\11272001\I852370A.raw

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210 <210> SEQ ID NO: 14
211 <211> LENGTH: 25
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Description of Artificial Sequence:
217      oligonucleotide used to determine the consensus
218      binding sequence of ZFHD1
220 <400> SEQUENCE: 14
221 agttattaat taagaatgtt aatta                                    25
224 <210> SEQ ID NO: 15
225 <211> LENGTH: 25
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence:
231      oligonucleotide used to determine the consensus
232      binding sequence of ZFHD1
234 <400> SEQUENCE: 15
235 gtgtgataat gagctggtcc gtccc                                    25
238 <210> SEQ ID NO: 16
239 <211> LENGTH: 25
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Description of Artificial Sequence:
245      oligonucleotide used to determine the consensus
246      binding sequence of ZFHD1
248 <400> SEQUENCE: 16
249 atattaaggc gtaattcgga caaga                                    25
252 <210> SEQ ID NO: 17
253 <211> LENGTH: 12
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus
259      binding sequence of ZFHD1
261 <220> FEATURE:
262 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
264 <400> SEQUENCE: 17
W--> 265 taattanggg ng                                             12
268 <210> SEQ ID NO: 18
269 <211> LENGTH: 12
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence: hybrid DNA
275      site
277 <220> FEATURE:
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Input Set : N:\Crf3\RULE60\09852370A.RAW.txt
Output Set: N:\CRF3\11272001\I852370A.raw

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      278 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
      280 <400> SEQUENCE: 18
W--> 281 aaatnntggg cg                                              12
      284 <210> SEQ ID NO: 19
      285 <211> LENGTH: 12
      286 <212> TYPE: DNA
      287 <213> ORGANISM: Artificial Sequence
      289 <220> FEATURE:
      290 <223> OTHER INFORMATION: Description of Artificial Sequence: predicted
      291      binding sequence
      293 <220> FEATURE:
      294 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
      296 <400> SEQUENCE: 19
W--> 297 cgcccannaa at                                              12
      300 <210> SEQ ID NO: 20
      301 <211> LENGTH: 10
      302 <212> TYPE: DNA
      303 <213> ORGANISM: human
      305 <400> SEQUENCE: 20
      306 atgcaaatga                                                10
      309 <210> SEQ ID NO: 21
      310 <211> LENGTH: 12
      311 <212> TYPE: DNA
      312 <213> ORGANISM: Artificial Sequence
      314 <220> FEATURE:
      315 <223> OTHER INFORMATION: Description of Artificial Sequence: hybrid binding
      316      site
      318 <400> SEQUENCE: 21
      319 taatgatggg cg                                              12
      322 <210> SEQ ID NO: 22
      323 <211> LENGTH: 63
      324 <212> TYPE: DNA
      325 <213> ORGANISM: Artificial Sequence
      327 <220> FEATURE:
      328 <223> OTHER INFORMATION: Description of Artificial Sequence: hybid binding
      329      site
      331 <220> FEATURE:
      332 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
      334 <400> SEQUENCE: 22
W--> 335 ggctgagtct gaacggatcc nnnnnnnnnn nnnnnnnnnn nnnnncctcg agactgagcg 60
      337 tcg                                                       63
      340 <210> SEQ ID NO: 23
      341 <211> LENGTH: 12
      342 <212> TYPE: DNA
      343 <213> ORGANISM: Artificial Sequence
      345 <220> FEATURE:
      346 <223> OTHER INFORMATION: Description of Artificial Sequence: probe
      348 <400> SEQUENCE: 23
      349 tcattatggg cg                                              12
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                    VERIFICATION SUMMARY              DATE: 11/27/2001
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                    Input Set : N:\Crf3\RULE60\09852370A.RAW.txt
                    Output Set: N:\CRF3\11272001\I852370A.raw

L:265 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:265 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:281 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:281 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:297 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:335 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:335 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:657 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:657 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:841 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:841 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:869 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:908 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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